What is Claimed is:

1. A screening and/or quantification method of one or more transcriptional factor(s) present in a cell or cell lysate, said method comprising the steps of:

a. binding to an insoluble solid support, double- stranded DNA sequence(s) at the concentration of at least 0.01 pmole/cm^2 of said solid support surface, said double-stranded DNA sequence comprising a specific sequence able to bind said transcriptional factor,

b. putting into contact said transcriptional factor with said bound double-stranded DNA sequence(s), and

c. identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) upon said double-stranded DNA sequence(s).

2. The method according to claim 1, wherein the transcriptional factor is present in solution at concentration lower than 20 nmolar (nM).

3. The method according to claim 1, wherein the specific sequence of the double-stranded DNA sequence(s) able to bind with the transcriptional factor(s) is located at a distance of at least about 6,8 nm from the surface of the solid support.

4. The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is a non radioactive resulting signal.

5. The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is obtained through an enzymatic reaction

6. The method according to any of the preceding claims 1 to 3, for the (possibly simultaneous) screening and/or quantification of multiple different transcriptional factors present in a same biological sample.

7. The method according to claim 1, for the screening and/or quantification of transcriptional factors selected from the group consisting of NF-KB, AP-1, CREB, SP-1, C/EBP, GR, HIF-1, Myc, NF-AT, Oct, TBP and CBF-1 or factors listed in table 1.

8. The method according to claim 1, for the screening and/or quantification of multiple different transcriptional factors upon a same support preferably upon the same multiwell plate.

9. The method according to claim 1, wherein the solid support is an array bearing upon at least 4 spots/cm2 of solid support surface, each spot containing double-stranded DNA sequence(s) for the binding of transcriptional factor(s).

10. The method according to claim 1, wherein the double-stranded DNA sequence(s) comprise(s), between the specific sequence able to bind the transcriptional factor(s) and the solid support, a spacer of at least about 13.5 nm.

11. The method according to claim 10, wherein said spacer is a double-stranded DNA nucleotide sequence of at least 20 base pairs, preferably at least 40 base pairs.

12. The method according to claim 1, wherein the double-stranded DNA sequence(s) are bound to a first member of a binding pair able to interact with a second member of said binding pair bound to the surface of the solid support.

13. The method according to claim 1, wherein the double-stranded DNA sequence(s) are covalently bound to the surface of the insoluble solid support.

14. The method according to claim 1, wherein the consensus sequence is repeated on the same molecule.

15. The method according to claim 1, wherein the double-stranded DNA sequences fixed on the support surface contain in part or totally one or several of the consensus DNA sequences presented in the table 1.

16. The method according to claim 1, wherein said transcriptional factor is the HIV integrase.

17. The method according to claim 1, comprising the step of identification of at least one characteristic specific of the transcriptional factor activation.

18. The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds able to bind to said transcriptional factor(s) or inhibit the binding of transcriptional factor(s) to the specific sequence upon the double-stranded DNA sequence(s) bound to said solid support.

19. The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds which modulate the binding and/or the activity of the said transcriptional factor(s) when they are put in contact with cells, tissues or organisms.

20. The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds which modulate the activity of enzyme(s) or protein(s) acting on transcrpitional factor(s) and then assayed for the binding to and/or activity of said transcriptional factor(s).

21. A method according to claim 1, which comprises the step of identification of transcriptional factor(s) and/or of peptides which are part of their active complex.

22. The method according to claim 1, which comprises the step of adding in the cell lysate an externally added

transcriptional factor or a compound which is able to bind to the consensus sequence.

23. A screening, diagnostic and/or quantification kit comprising reagents and media for performing the method according to claim 1.

24. The kit according to claim 23 for the screening and/or quantification of a transcriptional factor(s) or a compound able to bind to said transcriptional factor(s) or inhibit the binding of said transcriptional factor(s) to a specific nucleotide sequence, which comprises double-stranded DNA sequence(s) bound to an insoluble solid support at a concentration of at least about 0.01 pmole/cm^2 of solid support surface.

25. The kit according to claim 23, comprising a solid support bearing on its surface one or several double stranded DNA consensus sequences at a concentration of at least 0.01 pmole/cm^2 comprising in part or totally one or several of the consensus sequence(s) listed in table 1 allowing the binding of transcriptional factor(s) present in solution and their detection and/or quantification.

26. The kit according to claim 23, wherein the solid support is an array having at least 4 spot/cm^2 of solid support surface containing double-stranded DNA sequence(s) for the binding of the transcriptional factor(s).

27. The kit according to claim 23, wherein the double-stranded DNA sequence(s) comprises between the specific sequence able to bind the transcriptional factor(s) and the surface of the solid support, a spacer of at least about 13.5 nm.

28. The kit according to claim 23, wherein said spacer is a double-stranded DNA nucleotide sequence of at least 20 base pairs.

29. The kit according to the claim 27, wherein the spacer is a double-stranded DNA nucleotide sequence of at least 40 base pairs.

30. The kit according to claim 23, wherein the double-stranded DNA sequence(s) are bound to a first member of a binding pair (preferably biotin), able to interact with a second member of the binding pair (preferably streptavidin) bound to the surface of the solid support.

31. The kit according to claim 23, wherein the double-stranded DNA sequence(s) are covalently bound to the surface of the solid support.

32. The compounds identified and/or recovered by the method according to claim 19.

33. Pharmaceutical composition comprising an adequate pharmaceutical carrier and the unknown compound according to claim 32.

34. The method of Claim 12, wherein said first member of a binding pair is biotin.

35. The method of Claim 34, wherein said second member of a binding pair is streptavidin.